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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=6; day=24; hr=9; min=1; sec=31; ms=129;]

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Reviewer Comments:

For SEQ ID # 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, and 45, please reorder the numeric identifiers so the <300> series features come after all of the <200> series features.

For SEQ ID # 4, 6, 8, and 11, please remove the space found between the amino acids and the numbering.

For example in SEQ ID # 4:

Gly	Asp	Val	Phe	Thr	Met	Pro	Glu	Asp	Asp	Tyr	Trp	Ser	Tyr	Asp	Tyr
65						70				75					80

Val	Glu	Glu	Pro	Lys	Asn	Asn	Thr	Asn	Thr	Gly	Val	Gln	Pro	Glu	Asn
				85					90					95	

Thr	Ser	Pro	Pro	Gly	Asp	Leu	Asn	Pro	Arg	Thr	Asp	Gly	Thr	Leu	Lys
			100					105					110		

Remove the space between the amino acids and the numbers 85, 90, and 95. Look at the lines above and below for the correct format.

Application No: 10587756 Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-28 19:35:20.833
Finished: 2008-05-28 19:35:27.281
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 448 ms
Total Warnings: 3
Total Errors: 62
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (13)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (15)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (17)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (19)
W 402	Undefined organism found in <213> in SEQ ID (21)

[illegible]

Input Set:

Output Set:

Started: 2008-05-28 19:35:20.833
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Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 448 ms
Total Warnings: 3
Total Errors: 62
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (29)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (31)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (33)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (35)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (37)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (39)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (41)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (43)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID (45)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> Miyake, Masato
Yoshikawa, Tomohiro
Mikyake, Jun

<120> EVENT SEQUENCES

<130> 690121.409USPC

<140> US 10/587,756

<141> 2005-01-27

<150> PCT/JP2005/001151

<151> 2005-01-27

<150> JP 2004-24923

<151> 2004-01-30

<160> 46

<170> PatentIn version 3.1

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<220>

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<222> (1)..(1929)

<223> fibronectin 1

<400> 1

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ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag	96
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln	
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gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc	144
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser	
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Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln	
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Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr			
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Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala			
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Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu			
165	170	175	
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Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly			
180	185	190	
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Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr			
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Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg			
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His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp			
275	280	285	
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Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro			
290	295	300	
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Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met			
305	310	315	320

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Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu	
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ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt	1056
Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly	
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Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly	
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Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser	
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ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc	1200
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser	
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aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac	1248
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr	
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Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg	
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att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg	1440
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg	
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Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr	
485 490 495	
tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg	1536
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val	
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Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys	
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aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac	1632
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp	
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Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly	
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Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser	
580 585 590	
tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc	1824
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro	
595 600 605	
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Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser	
610 615 620	
aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt	1920
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35 40 45	
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln	
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Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly	
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Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr	

85

90

95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
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Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
 115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
 130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
 145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
 165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
 180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
 195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
 210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
 225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
 245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
 260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
 275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
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Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met

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Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu						
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Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly						
	340		345		350	
Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly						
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Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser						
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Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met						
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Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg						
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Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg						
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Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr						
	485		490		495	
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val						
	500		505		510	
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys						
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Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp						
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Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
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Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
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Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
 580 585 590

Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
 595 600 605

Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
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 Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe
 20 25 30
 atg gcc agc aag aag tgt cag tgt gac gag ctt tgc act tac tat cag 144
 Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln
 35 40 45
 agc tgc tgt gcc gac tac atg gag cag tgc aag ccc caa gta acg cgg 192
 Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg
 50 55 60

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Gly	Asp	Val	Phe	Thr	Met	Pro	Glu	Asp	Asp	Tyr	Trp	Ser	Tyr	Asp	Tyr	
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gtg	gag	gag	ccc	aag	aac	aat	acc	aac	acc	ggg	gtg	caa	ccc	gag	aac	288
Val	Glu	Glu	Pro	Lys	Asn	Asn	Thr	Asn	Thr	Gly	Val	Gln	Pro	Glu	Asn	
				85					90					95		
acc	tct	cca	ccc	ggg	gac	cta	aat	cct	cgg	acg	gac	ggc	act	cta	aag	336
Thr	Ser	Pro	Pro	Gly	Asp	Leu	Asn	Pro	Arg	Thr	Asp	Gly	Thr	Leu	Lys	
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ccg	aca	gcc	ttc	cta	gat	cct	gag	gaa	cag	cca	agc	acc	cca	gcg	cct	384
Pro	Thr	Ala	Phe	Leu	Asp	Pro	Glu	Glu	Gln	Pro	Ser	Thr	Pro	Ala	Pro	
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Asp	Ala	Phe	Thr	Asp	Leu	Lys	Asn	Gly	Ser	Leu	Phe	Ala	Phe	Arg	Gly	
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Phe	Thr	Arg	Ile	Asn	Cys	Gln	Gly	Lys	Thr	Tyr	Leu	Phe	Lys	Gly	Ser	
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Gln	Tyr	Trp	Arg	Phe	Glu	Asp	Gly	Val	Leu	Asp	Pro	Gly	Tyr	Pro	Arg	
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Asn	Ile	Ser	Glu	Gly	Phe	Ser	Gly	Ile	Pro	Asp	Asn	Val	Asp	Ala	Ala	
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ttc	gcc	ctt	cct	gcc	cac	cgt	tac	agt	ggc	cgg	gaa	agg	gtc	tac	ttc	816
Phe	Ala	Leu	Pro	Ala	His	Arg	Tyr	Ser	Gly	Arg	Glu	Arg	Val	Tyr	Phe	
			260					265					270			
ttc	aag	ggg	aag	cag	tac	tgg	gag	cac	gaa	ttt	cag	cag	caa	ccc		

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Ala Leu Leu Gln Arg Asp Ser Trp Glu Asn Ile Phe Glu Leu Leu Phe	
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Trp Gly Arg Ser Ser Asp Gly Ala Arg Glu Pro Gln Phe Ile Ser Arg	
325 330 335	
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Asn Trp His Gly Val Pro Gly Lys Val Asp Ala Ala Met Ala Gly Arg	
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Ile Tyr Val Thr Gly Ser Leu Ser His Ser Ala Gln Ala Lys Lys Gln	
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